RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/527,101_
Source: _PCT_
Date Processed by STIC: _2/13/06_

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RAW SEQUENCE LISTING   DATE: 02/13/2006
PATENT APPLICATION: **US/10/527,101**   TIME: 13:10:11

Input Set : **E:\Sequence Listing P1978R1.txt**
Output Set: **N:\CRF4\02132006\J527101.raw**

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 3 <110> APPLICANT: SARAH C. BODARY
 4        HILARY CLARK
 5        JANET K. JACKMAN
 6        JILL R. SCHOENFELD
 7        WILLIAM I. WOOD
 8        THOMAS D. WU
10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF PSORIASIS
12 <130> FILE REFERENCE: P1978R1-US
14 <140> CURRENT APPLICATION NUMBER: US 10/527,101
15 <141> CURRENT FILING DATE: 2005-03-09
17 <150> PRIOR APPLICATION NUMBER: PCT/US03/28362
18 <151> PRIOR FILING DATE: 2005-09-10
20 <150> PRIOR APPLICATION NUMBER: US 60/410,242
21 <151> PRIOR FILING DATE: 2002-09-11
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25 <210> SEQ ID NO: 1
26 <211> LENGTH: 732
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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35  ttggccttat gtgcttcctg agtattatta ttactacagt ttgcattatt 150
37  atgatagcca catggtccaa gcatgctaaa cctgtggcat gttcagggga 200
39  ctggcttgga gtgagagata agtgtttcta tttttctgat gataccagaa 250
41  attggacagc cagtaaaata ttttgtagtt tgcagaaagc agaacttgct 300
43  cagattgata cacaagaaga catggaattt ttgaagaggt acgcaggaac 350
45  tgatatgcac tggattggac taagcaggaa acaaggagat tcttggaaat 400
47  ggacaaatgg caccacattc aatggttggc catcaaactc caaatggtct 450
49  tgcaactgga gcctccgaca atggcttctt ctgctgggac cccttagata 500
51  ggcctctgag ggagctctga ctgccgtttc cccaaaacaa tgtcccctgt 550
53  cagcaggaag cagttaaatc agtcttcatc cttatcctta atataacggc 600
55  agttagatgt acttctttag agggagtaaa tttatcaatt cagagcaatt 650
57  catcctcctc tttccatctt tgattcacag ttaataggct ataaattttg 700
59  ataatgtaga ataaactaca gaaaacttct tg 732
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62 <211> LENGTH: 160
63 <212> TYPE: PRT
64 <213> ORGANISM: Homo sapiens
66 <400> SEQUENCE: 2
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70  His Arg Ile Val Pro Lys Leu Ile Gln Asn Trp Lys Ile Gly Leu
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73   Met Cys Phe Leu Ser Ile Ile Ile Thr Thr Val Cys Ile Ile Met
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76   Ile Ala Thr Trp Ser Lys His Ala Lys Pro Val Ala Cys Ser Gly
77                      50                  55                  60
79   Asp Trp Leu Gly Val Arg Asp Lys Cys Phe Tyr Phe Ser Asp Asp
80                      65                  70                  75
82   Thr Arg Asn Trp Thr Ala Ser Lys Ile Phe Cys Ser Leu Gln Lys
83                      80                  85                  90
85   Ala Glu Leu Ala Gln Ile Asp Thr Gln Glu Asp Met Glu Phe Leu
86                      95                  100                 105
88   Lys Arg Tyr Ala Gly Thr Asp Met His Trp Ile Gly Leu Ser Arg
89                      110                 115                 120
91   Lys Gln Gly Asp Ser Trp Lys Trp Thr Asn Gly Thr Thr Phe Asn
92                      125                 130                 135
94   Gly Trp Pro Ser Asn Ser Lys Trp Ser Cys Asn Trp Ser Leu Arg
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102  <212> TYPE: DNA
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110  ttttcttctt acacagtgtc tgagaacatt tacattatag ataagtagta 150
112  catggtggat aacttctact tttaggagga ctactctctt ctgacagtcc 200
114  tagactggtc ttctacacta agacaccatg aaggagtatg tgctcctatt 250
116  attcctggct ttgtgctctg ccaaaccctt ctttagccct tcacacatcg 300
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120  gatgatgatg atgatgatga tgatgatgat gatgaggaca actctctttt 400
122  tccaacaaga gagccaagaa gccatttttt tccatttgat ctgtttccaa 450
124  tgtgtccatt tggatgtcag tgctattcac gagttgtaca ttgctcagat 500
126  ttaggtttga cctcagtccc aaccaacatt ccatttgata ctcgaatgct 550
128  tgatcttcaa aacaataaaa ttaaggaaat caaagaaaat gattttaaag 600
130  gactcacttc actttatggt ctgatcctga acaacaacaa gctaacgaag 650
132  attcacccaa aagcctttct aaccacaaag aagttgcgaa ggctgtatct 700
134  gtcccacaat caactaagtg aaataccact taatcttccc aaatcattag 750
136  cagaactcag aattcatgaa aataaagtta agaaaataca aaaggacaca 800
138  ttcaaaggaa tgaatgcttt acacgttttg gaaatgagtg caaaccctct 850
140  tgataataat gggatagagc caggggcatt tgaaggggtg acggtgttcc 900
142  atatcagaat tgcagaagca aaactgacct cagttcctaa aggcttacca 950
144  ccaactttat tggagcttca cttagattat aataaaattt caacagtgga 1000
146  acttgaggat tttaaacgat acaaagaact acaaaggctg ggcctaggaa 1050
148  acaacaaaat cacagatatc gaaatggga gtcttgctaa cataccacgt 1100
150  gtgagagaaa tacatttgga aaacaataaa ctaaaaaaaa tcccttcagg 1150
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154  ttgcaagagt gggagtaaat gacttctgtc aacagtgcc aaagatgaag 1250
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156  aaatctttat acagtgcaat aagtttattc aacaacccgg tgaaatactg 1300
158  ggaaatgcaa cctgcaacat ttcgttgtgt tttgagcaga atgagtgttc 1350
160  agcttgggaa ctttggaatg taataattag taattggtaa tgtccattta 1400
162  atataagatt caaaaatccc tacatttgga atacttgaac tctattaata 1450
164  atggtagtat tatatataca agcaaatatc tattctcaag tggtaagtcc 1500
166  actgacttat tttatgacaa gaaatttcaa cggaattttg ccaaactatt 1550
168  gatacataag ggttgagaga aacaagcatc tattgcagtt tcttttttgcg 1600
170  tacaaatgat cttacataaa tctcatgctt gaccattcct ttcttcataa 1650
172  caaaaaagta agatattcgg tatttaacac tttgttatca agcacatttt 1700
174  aaaaagagct gtactgtaaa tggaatgctt gacttagcaa aatttgtgct 1750
176  ctttcatttg ctgttagaaa aacagaatta acaaagacag taatgtgaag 1800
178  agtgcattac actattctta ttctttagta gcttgggtag tactgtaata 1850
180  ttttttaatca tcttaaagta tgatttgata taatcttatt gaaattacct 1900
182  tatcatgtct tagagcccgt ctttatgttt aaaactaatt tcttaaaata 1950
184  aagccttcag taaatgttca ttaccaactt gataaatgct actcataaga 2000
186  gctggtttgg ggctatagca tatgcttttt tttttttaat tattacctga 2050
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192  gctatataac attgccactt caactctaag gaatacttt gagatatccc 2200
194  tttggaagac cttgcttgga agagcctgga cactaacaat tctacaccaa 2250
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200  tctatataaa tgctcagagt tctttatgta tttcttattg gcattcaaca 2400
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216                  20                  25                  30
218  Leu Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp Asp
219                  35                  40                  45
221  Asp Asp Asp Asp Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr
222                  50                  55                  60
224  Arg Glu Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met
225                  65                  70                  75
227  Cys Pro Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser
228                  80                  85                  90
230  Asp Leu Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr
231                  95                  100                 105
233  Arg Met Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu
234                  110                 115                 120
236  Asn Asp Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn
237                  125                 130                 135
239  Asn Asn Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr
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242  Lys Lys Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu
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246                    170              175                180
248  Glu Asn Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met
249                    185              190                195
251  Asn Ala Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn
252                    200              205                210
254  Asn Gly Ile Glu Pro Gly Ala Phe Glu Gly Val Thr Val Phe His
255                    215              220                225
257  Ile Arg Ile Ala Glu Ala Lys Leu Thr Ser Val Pro Lys Gly Leu
258                    230              235                240
260  Pro Pro Thr Leu Leu Glu Leu His Leu Asp Tyr Asn Lys Ile Ser
261                    245              250                255
263  Thr Val Glu Leu Glu Asp Phe Lys Arg Tyr Lys Glu Leu Gln Arg
264                    260              265                270
266  Leu Gly Leu Gly Asn Asn Lys Ile Thr Asp Ile Glu Asn Gly Ser
267                    275              280                285
269  Leu Ala Asn Ile Pro Arg Val Arg Glu Ile His Leu Glu Asn Asn
270                    290              295                300
272  Lys Leu Lys Lys Ile Pro Ser Gly Leu Pro Glu Leu Lys Tyr Leu
273                    305              310                315
275  Gln Ile Ile Phe Leu His Ser Asn Ser Ile Ala Arg Val Gly Val
276                    320              325                330
278  Asn Asp Phe Cys Pro Thr Val Pro Lys Met Lys Lys Ser Leu Tyr
279                    335              340                345
281  Ser Ala Ile Ser Leu Phe Asn Asn Pro Val Lys Tyr Trp Glu Met
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300  attccagcag cgccttaccg cgcagcccga agattcacta tggtgaaaat 150
302  cgccttcaat acccctaccg ccgtgcaaaa ggaggaggcg cggcaagacg 200
304  tggaggcccct cctgagccgc acggtcagaa ctcagatact gaccggcaag 250
306  gagctccgag ttgccaccca ggaaaaagag ggctcctctg ggagatgtat 300
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310  gagcctgcat ttacaagtac ttcatgccca agagcaccat ttaccgtgga 400
312  gagatgtgct tttttgattc tgaggatcct gcaaattccc ttcgtggagg 450
314  agagcctaac ttcctgcctg tgactgagga ggctgacatt cgtgaggatg 500
316  acaacattgc aatcattgat gtgcctgtcc ccagtttctc tgatagtgac 550
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322   tgcctccaaa aaatctggta gagctctttg gcaaactggc gagtggcaga 700
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326   aattcgtgat gttagtaacc ttggcatctt tatttaccaa ctttgcaata 800
328   acagaaagtc cttccgcctt cgtcgcagag acctcttgct gggtttcaac 850
330   aaacgtgcca ttgataaatg ctggaagatt agacacttcc ccaacgaatt 900
332   tattgttgag accaagatct gtcaagagta agaggcaaca gatagagtgt 950
334   ccttggtaat aagaagtcag agatttacaa tatgacttta acattaaggt 1000
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352   Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
353                   35                  40                  45
355   Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu
356                   50                  55                  60
358   Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr
359                   65                  70                  75
361   Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys
362                   80                  85                  90
364   Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu
365                   95                  100                 105
367   Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp
368                   110                 115                 120
370   Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp
371                   125                 130                 135
373   Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr
374                   140                 145                 150
376   Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu
377                   155                 160                 165
379   Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe
380                   170                 175                 180
382   Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val
383                   185                 190                 195
385   Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn
386                   200                 205                 210
388   Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe
389                   215                 220                 225
391   Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
392                   230                 235                 240
394   Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile
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VERIFICATION SUMMARY   DATE: 02/13/2006
PATENT APPLICATION: **US/10/527,101** TIME: 13:10:12

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